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ttgattattg aagctcgcaa gggtaatact cagccagctt tgtcatggtt tgcactaaaa   180

tcagcactca gcaataacca aattgctgac tggttacaga ttgccttatg ggccgggcaa   240

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tggcaaaagg cgctctctct ggagccgcaa aataaggatt atcaacgggg acaaatttta   420

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gctgcattag aaattctgtg gcacgataac ccagaccgca ctgcccagta ccagcgtatt   840

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gaaatgacag ccagagagct tgcttataac gcaccaggaa atcagggact gcgcattgat    1320

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ctgtattacg aacaaaatac agaacacgat accccatact acaaccctat aaaaacgttc    2160

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gagcaaatat tcagcgcagg tgttggtgcc tcctggcaaa aacattatgg cacggatgtc    2280

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acgctacgct gggaaaaacg accttatgac ggtgacagag aacacaactt atacgttgaa    2400

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<211> 807
<212> PRT
<213> Escherichia coli

<400> 2

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2

Ala Val Asn Asn Ala Tyr Asp Ala Leu Ile Ile Glu Ala Arg Lys Gly
        35   40   45

Asn Thr Gln Pro Ala Leu Ser Trp Phe Ala Leu Lys Ser Ala Leu Ser
        50   55   60

Asn Asn Gln Ile Ala Asp Trp Leu Gln Ile Ala Leu Trp Ala Gly Gln
65   70   75   80

Asp Lys Gln Val Ile Thr Val Tyr Asn Arg Tyr Arg His Gln Gln Leu
                85   90   95

Pro Ala Arg Gly Tyr Ala Ala Val Ala Val Ala Tyr Arg Asn Leu Gln
            100   105   110

Gln Trp Gln Asn Ser Leu Thr Leu Trp Gln Lys Ala Leu Ser Leu Glu
        115   120   125

Pro Gln Asn Lys Asp Tyr Gln Arg Gly Gln Ile Leu Thr Leu Ala Asp
    130   135   140

Ala Gly His Tyr Asp Thr Ala Leu Val Lys Leu Lys Gln Leu Asn Ser
145   150   155   160

Gly Ala Pro Asp Lys Ala Asn Leu Leu Ala Glu Ala Tyr Ile Tyr Lys
            165   170   175

Leu Ala Gly Arg His Gln Asp Glu Leu Arg Ala Met Thr Glu Ser Leu
            180   185   190

Pro Glu Asn Ala Ser Thr Gln Gln Tyr Pro Thr Glu Tyr Val Gln Ala
        195   200   205

Leu Arg Asn Asn Gln Leu Ala Ala Ala Ile Asp Asp Ala Asn Leu Thr
    210   215   220

Pro Asp Ile Arg Ala Asp Ile His Ala Glu Leu Val Arg Leu Ser Phe
225   230   235   240

Met Pro Thr Arg Ser Glu Ser Glu Arg Tyr Ala Ile Ala Asp Arg Ala
            245   250   255

Leu Ala Gln Tyr Ala Ala Leu Glu Ile Leu Trp His Asp Asn Pro Asp

3

Arg Thr Ala Gln Tyr Gln Arg Ile Gln Val Asp His Leu Gly Ala Leu
        275   280   285

Leu Thr Arg Asp Arg Tyr Lys Asp Val Ile Ser His Tyr Gln Arg Leu
        290   295   300

Lys Lys Thr Gly Gln Ile Ile Pro Pro Trp Gly Gln Tyr Trp Val Ala
305   310   315   320

Ser Ala Tyr Leu Lys Asp His Gln Pro Lys Lys Ala Gln Ser Ile Met
                325   330   335

Thr Glu Leu Phe Tyr His Lys Glu Thr Ile Ala Pro Asp Leu Ser Asp
                340   345   350

Glu Glu Leu Ala Asp Leu Phe Tyr Ser His Leu Glu Ser Glu Asn Tyr
        355   360   365

Pro Gly Ala Leu Thr Val Thr Gln His Thr Ile Asn Thr Ser Pro Pro
        370   375   380

Phe Leu Arg Leu Met Gly Thr Pro Thr Ser Ile Pro Asn Asp Thr Trp
385   390   395   400

Leu Gln Gly His Ser Phe Leu Ser Thr Val Ala Lys Tyr Ser Asn Asp
                405   410   415

Leu Pro Gln Ala Glu Met Thr Ala Arg Glu Leu Ala Tyr Asn Ala Pro
                420   425   430

Gly Asn Gln Gly Leu Arg Ile Asp Tyr Ala Ser Val Leu Gln Ala Arg
                435   440   445

Gly Trp Pro Arg Ala Ala Glu Asn Glu Leu Lys Lys Ala Glu Val Ile
        450   455   460

Glu Pro Arg Asn Ile Asn Leu Glu Val Glu Gln Ala Trp Thr Ala Leu
465   470   475   480

Thr Leu Gln Glu Trp Gln Gln Ala Ala Val Leu Thr His Asp Val Val
                485   490   495

Glu Arg Glu Pro Gln Asp Pro Gly Val Val Arg Leu Lys Arg Ala Val
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500   505   510

Asp Val His Asn Leu Ala Glu Leu Arg Ile Ala Gly Ser Thr Gly Ile
        515   520   525

Asp Ala Glu Gly Pro Asp Ser Gly Lys His Asp Val Asp Leu Thr Thr
        530   535   540

Ile Val Tyr Ser Pro Pro Leu Lys Asp Asn Trp Arg Gly Phe Ala Gly
545   550   555   560

Phe Gly Tyr Ala Asp Gly Gln Phe Ser Glu Gly Lys Gly Ile Val Arg
                565   570   575

Asp Trp Leu Ala Gly Val Glu Trp Arg Ser Arg Asn Ile Trp Leu Glu
            580   585   590

Ala Glu Tyr Ala Glu Arg Val Phe Asn His Glu His Lys Pro Gly Ala
        595   600   605

Arg Leu Ser Gly Trp Tyr Asp Phe Asn Asp Asn Trp Arg Ile Gly Ser
    610   615   620

Gln Leu Glu Arg Leu Ser His Arg Val Pro Leu Arg Ala Met Lys Asn
625   630   635   640

Gly Val Thr Gly Asn Ser Ala Gln Ala Tyr Val Arg Trp Tyr Gln Asn
                645   650   655

Glu Arg Arg Lys Tyr Gly Val Ser Trp Ala Phe Thr Asp Phe Ser Asp
                660   665   670

Ser Asn Gln Arg His Glu Val Ser Leu Glu Gly Gln Glu Arg Ile Trp
            675   680   685

Ser Ser Pro Tyr Leu Ile Val Asp Phe Leu Pro Ser Leu Tyr Tyr Glu
            690   695   700

Gln Asn Thr Glu His Asp Thr Pro Tyr Tyr Asn Pro Ile Lys Thr Phe
705   710   715   720

Asp Ile Val Pro Ala Phe Glu Ala Ser His Leu Leu Trp Arg Ser Tyr
                725   730   735

Glu Asn Ser Trp Glu Gln Ile Phe Ser Ala Gly Val Gly Ala Ser Trp

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                740                    745                     750


    Gln Lys His Tyr Gly Thr Asp Val Val Thr Gln Leu Gly Tyr Gly Gln
         755                    760                     765


    Arg Ile Ser Trp Asn Asp Val Ile Asp Ala Gly Ala Thr Leu Arg Trp
         770                    775                     780


    Glu Lys Arg Pro Tyr Asp Gly Asp Arg Glu His Asn Leu Tyr Val Glu
    785                    790                     795                     800


    Phe Asp Met Thr Phe Arg Phe
                     805


    <210>  3
    <211>  2031
    <212>  DNA
    <213>  Escherichia coli

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    atgctcaccg cgtgcattag ccagtcaaga acatcattta taccgccaca ggatcgcgaa     120

    tctttactcg ccgagcaacc gtggccgcat aatggttttg tagcgatttc atggcataac     180

    gttgaagacg aagctgccga ccagcgtttt atgtcagtgc ggacatcagc actgcgtgaa     240

    caatttgcct ggctgcgcga gaacggttat caaccggtca gtattgctca aattcgtgaa     300

    gcacatcgag gaggaaaacc gctaccggaa aaagctgtag tgctgacttt tgatgacggc     360

    taccagagtt tttatacccg cgtcttccca attcttcagg ccttccagtg gcctgctgta     420

    tgggcccccg tcggcagttg ggtcgatacg ccagcggata aacaagtaaa atttggcgat     480

    gagttggtcg atcgagaata ttttgccacg tggcaacaag tgcgagaagt tgcgcgttcc     540

    cggctcgttg agctcgcttc tcatacatgg aattctcact acggtattca ggctaatgcc     600

    accggcagct tattgcctgt atatgtaaat cgtgcatatt ttactgacca cgcacggtat     660

    gaaaccgcag cagaataccg ggaaagaatt cgtctggatg ctgtaaaaat gacggaatac     720

    ctgcgtacaa aggttgaggt aaatccacac gtttttgttt ggccttatgg cgaagcgaat     780

    ggcatagcga tagaggaatt aaaaaaactc ggttatgaca tgttcttcac ccttgaatca     840

    ggtttggcaa atgcgtcgca attggattcc attccgcggg tattaatcgc caataatccc     900

    tcattaaaag agtttgccca gcaaattatt accgtacagg aaaaatcacc acaacggata     960

    atgcatatcg atcttgatta cgtttatgac gaaaacctcc agcaaatgga tcgcaatatt    1020

    gatgtgctaa ttcagcgggt gaaagatatg caaatatcaa ccgtgtattt gcaggcattt    1080
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atgaaagcag atattttag tcgggttgcc tggcaattac gtacccgctc aggtgtaaac    1200

atctatgcgt ggatgccggt attaagctgg gatttagatc ccacattaac gcgagtaaaa    1260

tacttaccaa caggggagaa aaaagcacaa attcatcctg aacaatatca ccgtctctct    1320

cctttcgatg acagagtcag agcacaagtt ggcatgttat atgaagatct tgccggacat    1380

gctgctttg atggcatatt gttccacgat gatgctttgc tttcagatta tgaagatgcc    1440

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tatgctgatt tcctaaaaag ctatgactgg accgctatta tggctatgcc ttatctggaa    1740

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atccctcagg ctaaagacaa atctatttta gaattacagg cacaaaactg gcagaaaaat    1860

ggtcagcatc aggctatttc ttcgcaacaa ctcgctcact ggatgagcct attacaactg    1920

aatggagtga aaaactatgg ttattatccc gacaattttc tgcataacca acctgaaata    1980

gaccttattc gtcctgagtt ttcaacagcc tggtatccga aaaatgatta a    2031


<210>   4
<211>   672
<212>   PRT
<213>   Escherichia coli

<400>   4

Met Leu Arg Asn Gly Asn Lys Tyr Leu Leu Met Leu Val Ser Ile Ile
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Met Leu Thr Ala Cys Ile Ser Gln Ser Arg Thr Ser Phe Ile Pro Pro
            20                  25                  30


Gln Asp Arg Glu Ser Leu Leu Ala Glu Gln Pro Trp Pro His Asn Gly
        35                  40                  45


Phe Val Ala Ile Ser Trp His Asn Val Glu Asp Glu Ala Ala Asp Gln
    50                  55                  60


Arg Phe Met Ser Val Arg Thr Ser Ala Leu Arg Glu Gln Phe Ala Trp
65                  70                  75                  80
```

7

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Leu Arg Glu Asn Gly Tyr Gln Pro Val Ser Ile Ala Gln Ile Arg Glu
                85                  90                  95

Ala His Arg Gly Gly Lys Pro Leu Pro Glu Lys Ala Val Val Leu Thr
            100                 105                 110

Phe Asp Asp Gly Tyr Gln Ser Phe Tyr Thr Arg Val Phe Pro Ile Leu
            115                 120                 125

Gln Ala Phe Gln Trp Pro Ala Val Trp Ala Pro Val Gly Ser Trp Val
    130                 135                 140

Asp Thr Pro Ala Asp Lys Gln Val Lys Phe Gly Asp Glu Leu Val Asp
145                 150                 155                 160

Arg Glu Tyr Phe Ala Thr Trp Gln Gln Val Arg Glu Val Ala Arg Ser
            165                 170                 175

Arg Leu Val Glu Leu Ala Ser His Thr Trp Asn Ser His Tyr Gly Ile
            180                 185                 190

Gln Ala Asn Ala Thr Gly Ser Leu Leu Pro Val Tyr Val Asn Arg Ala
    195                 200                 205

Tyr Phe Thr Asp His Ala Arg Tyr Glu Thr Ala Ala Glu Tyr Arg Glu
    210                 215                 220

Arg Ile Arg Leu Asp Ala Val Lys Met Thr Glu Tyr Leu Arg Thr Lys
225                 230                 235                 240

Val Glu Val Asn Pro His Val Phe Val Trp Pro Tyr Gly Glu Ala Asn
            245                 250                 255

Gly Ile Ala Ile Glu Glu Leu Lys Lys Leu Gly Tyr Asp Met Phe Phe
            260                 265                 270

Thr Leu Glu Ser Gly Leu Ala Asn Ala Ser Gln Leu Asp Ser Ile Pro
    275                 280                 285

Arg Val Leu Ile Ala Asn Asn Pro Ser Leu Lys Glu Phe Ala Gln Gln
    290                 295                 300

Ile Ile Thr Val Gln Glu Lys Ser Pro Gln Arg Ile Met His Ile Asp
305                 310                 315                 320
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8

Leu Asp Tyr Val Tyr Asp Glu Asn Leu Gln Gln Met Asp Arg Asn Ile
            325   330   335

Asp Val Leu Ile Gln Arg Val Lys Asp Met Gln Ile Ser Thr Val Tyr
            340   345   350

Leu Gln Ala Phe Ala Asp Pro Asp Gly Asp Gly Leu Val Lys Glu Val
            355   360   365

Trp Phe Pro Asn Arg Leu Leu Pro Met Lys Ala Asp Ile Phe Ser Arg
    370   375   380

Val Ala Trp Gln Leu Arg Thr Arg Ser Gly Val Asn Ile Tyr Ala Trp
385   390   395   400

Met Pro Val Leu Ser Trp Asp Leu Asp Pro Thr Leu Thr Arg Val Lys
                405   410   415

Tyr Leu Pro Thr Gly Glu Lys Lys Ala Gln Ile His Pro Glu Gln Tyr
                420   425   430

His Arg Leu Ser Pro Phe Asp Asp Arg Val Arg Ala Gln Val Gly Met
            435   440   445

Leu Tyr Glu Asp Leu Ala Gly His Ala Ala Phe Asp Gly Ile Leu Phe
    450   455   460

His Asp Asp Ala Leu Leu Ser Asp Tyr Glu Asp Ala Ser Ala Pro Ala
465   470   475   480

Ile Thr Ala Tyr Gln Gln Ala Gly Phe Ser Gly Ser Leu Ser Glu Ile
                485   490   495

Arg Gln Asn Pro Glu Gln Phe Lys Gln Trp Ala Arg Phe Lys Ser Arg
                500   505   510

Ala Leu Thr Asp Phe Thr Leu Glu Leu Ser Ala Arg Val Lys Ala Ile
            515   520   525

Arg Gly Pro His Ile Lys Thr Ala Arg Asn Ile Phe Ala Leu Pro Val
    530   535   540

Ile Gln Pro Glu Ser Glu Ala Trp Phe Ala Gln Asn Tyr Ala Asp Phe
545   550   555   560

9

Leu Lys Ser Tyr Asp Trp Thr Ala Ile Met Ala Met Pro Tyr Leu Glu
            565   570   575

Gly Val Ala Glu Lys Ser Ala Asp Gln Trp Leu Ile Gln Leu Thr Asn
            580   585   590

Gln Ile Lys Asn Ile Pro Gln Ala Lys Asp Lys Ser Ile Leu Glu Leu
            595   600   605

Gln Ala Gln Asn Trp Gln Lys Asn Gly Gln His Gln Ala Ile Ser Ser
    610   615   620

Gln Gln Leu Ala His Trp Met Ser Leu Leu Gln Leu Asn Gly Val Lys
625   630   635   640

Asn Tyr Gly Tyr Tyr Pro Asp Asn Phe Leu His Asn Gln Pro Glu Ile
            645   650   655

Asp Leu Ile Arg Pro Glu Phe Ser Thr Ala Trp Tyr Pro Lys Asn Asp
            660   665   670

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<211> 1380
<212> DNA
<213> Escherichia coli

<400> 5
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cagcgttatg agaacattga agttattgcc gtaaatgacg gttcaacaga taaaacccgt   360

gccatcctgg atcgcatggc tgcacaaatt ccccatttgc gggtcattca tctggcgcaa   420

aaccagggga aagccattgc gcttaaaacc ggagctgccg cggcgaaaag tgaatatctg   480

gtgtgcattg atggcgatgc gttattagac cgcgatgcgg cggcatatat tgtggaaccg   540

atgttgtaca acccgcgtgt gggtgccgta accggtaatc ctcgtattcg aacacgttct   600

accctggtgg gtaaaattca ggttggcgag tattcctcaa ttattggttt gatcaagcga   660

acccagcgta tctatggaaa cgtatttacc gtttccggtg ttattgccgc atttcgtcgc   720

agcgccctgg cagaagtggg ttactggagt gacgatatga tcaccgaaga tattgatatt   780

10

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agctggaagc tgcagttgaa tcagtggacg atttttttacg agccacgggc actgtgctgg      840

atattaatgc ctgaaacgtt aaaagggctg tggaaacagc gcctgcgctg ggctcagggc      900

ggtgcagaag tattcctcaa aaatatgaca aggttgtggc gcaaagaaaa ctttcgaatg      960

tggccgctgt tttttgaata ctgcctgacg acaatatggg ccttcacctg cctggtcggt     1020

ttcattattt acgcagtcca acttgccggt gtaccgttaa atattgaatt gacacatatc     1080

gctgcgacac atactgccgg aatattattg tgtacgttat gtttactgca atttattgtc     1140

agcctgatga tcgagaatcg ctatgagcat aatctgactt catcgctttt ctggattatt     1200

tggttcccgg ttattttctg gatgctgagc ctggcaacga cattggtatc atttacacga     1260

gtcatgttga tgcctaaaaa gcaacgcgcc cgttgggtaa gtcccgatcg cgggattctg     1320

agaggttaat atgaacaatt taattattac gacccgacaa tcaccagtac gttactggt      1380
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<210> 6
<211> 445
<212> PRT
<213> Escherichia coli

<400> 6

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Ile Pro Leu Cys Val Ala Tyr Phe His Ser Gly Glu Leu Met Met Arg
            20   25   30

Phe Val Phe Phe Trp Pro Phe Phe Met Ser Ile Met Trp Ile Val Gly
            35   40   45

Gly Val Tyr Phe Trp Val Tyr Arg Glu Arg His Trp Pro Trp Gly Glu
    50   55   60

Asn Ala Pro Ala Pro Gln Leu Lys Asp Asn Pro Ser Ile Ser Ile Ile
65   70   75   80

Ile Pro Cys Phe Asn Glu Glu Lys Asn Val Glu Glu Thr Ile His Ala
                85   90   95

Ala Leu Ala Gln Arg Tyr Glu Asn Ile Glu Val Ile Ala Val Asn Asp
                100   105   110

Gly Ser Thr Asp Lys Thr Arg Ala Ile Leu Asp Arg Met Ala Ala Gln
        115   120   125

                                11
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Ile Pro His Leu Arg Val Ile His Leu Ala Gln Asn Gln Gly Lys Ala
    130                 135                 140

Ile Ala Leu Lys Thr Gly Ala Ala Ala Lys Ser Glu Tyr Leu Val
145                 150                 155                 160

Cys Ile Asp Gly Asp Ala Leu Leu Asp Arg Asp Ala Ala Ala Tyr Ile
                165                 170                 175

Val Glu Pro Met Leu Tyr Asn Pro Arg Val Gly Ala Val Thr Gly Asn
                180                 185                 190

Pro Arg Ile Arg Thr Arg Ser Thr Leu Val Gly Lys Ile Gln Val Gly
                195                 200                 205

Glu Tyr Ser Ser Ile Ile Gly Leu Ile Lys Arg Thr Gln Arg Ile Tyr
    210                 215                 220

Gly Asn Val Phe Thr Val Ser Gly Val Ile Ala Ala Phe Arg Arg Ser
225                 230                 235                 240

Ala Leu Ala Glu Val Gly Tyr Trp Ser Asp Asp Met Ile Thr Glu Asp
                245                 250                 255

Ile Asp Ile Ser Trp Lys Leu Gln Leu Asn Gln Trp Thr Ile Phe Tyr
                260                 265                 270

Glu Pro Arg Ala Leu Cys Trp Ile Leu Met Pro Glu Thr Leu Lys Gly
                275                 280                 285

Leu Trp Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Val Phe
    290                 295                 300

Leu Lys Asn Met Thr Arg Leu Trp Arg Lys Glu Asn Phe Arg Met Trp
305                 310                 315                 320

Pro Leu Phe Phe Glu Tyr Cys Leu Thr Thr Ile Trp Ala Phe Thr Cys
                325                 330                 335

Leu Val Gly Phe Ile Ile Tyr Ala Val Gln Leu Ala Gly Val Pro Leu
                340                 345                 350

Asn Ile Glu Leu Thr His Ile Ala Ala Thr His Thr Ala Gly Ile Leu
    355                 360                 365
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Leu Cys Thr Leu Cys Leu Leu Gln Phe Ile Val Ser Leu Met Ile Glu
    370   375   380

Asn Arg Tyr Glu His Asn Leu Thr Ser Ser Leu Phe Trp Ile Ile Trp
385   390   395   400

Phe Pro Val Ile Phe Trp Met Leu Ser Leu Ala Thr Thr Leu Val Ser
                405   410   415

Phe Thr Arg Val Met Leu Met Pro Lys Lys Gln Arg Ala Arg Trp Val
            420   425   430

Ser Pro Asp Arg Gly Ile Leu Arg Gly Met Asn Asn Leu
        435   440   445

<210> 7
<211> 30
<212> DNA
<213> Escherichia coli

<400> 7
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<210> 8
<211> 31
<212> DNA
<213> Escherichia coli

<400> 8
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<210> 9
<211> 7500
<212> DNA
<213> Escherichia coli

<400> 9
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ttgattattg aagctcgcaa gggtaatact cagccagctt tgtcatggtt tgcactaaaa   180

tcagcactca gcaataacca aattgctgac tggttacaga ttgccttatg ggccgggcaa   240

gataaacagg ttattaccgt ttacaaccgc taccgtcatc agcaattacc agcgcgtggt   300

tatgcagctg tcgccgtcgc ttatcgtaac ctgcaacaat ggcaaaactc gcttacactg   360

tggcaaaagg cgctctctct ggagccgcaa aataaggatt atcaacgggg acaaatttta   420

accctggcag atgctggtca ctatgatact gcgctggtta aacttaagca gcttaactct   480

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ggagcaccgg acaaagccaa tttactcgca gaagcctata tctataaact ggcggggcgt    540

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14

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15

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16

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